

SEQUENCE LISTING

RECEIVED

JUL 3 1 2001

TECH CENTER 1600/2900

<110> Parkar, Christi L. Moore, Kevin W.

Murgolo, Nicholas J. Bazan, J. Fernando

- <120> HUMAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
- <130> DX0804K
- <140> 09/265,540
- <141> 1999-03-08
- <150> 60/077,329
- <151> 1999-03-09
- <160> 6
- <170> PatentIn version 3.1
- <210> 1
- <211> 1381
- <212> DNA
- <213> Homo sapiens
- <220>
- <221> CDS
- <222> (132)..(1064)
- <223>
- <220>
- <221> misc feature
- <222> (567)..(567)
- <223> unknown nucleotide
- <220>
- <221> misc_feature
- <222> (573)..(573)
- <223> unknown nucleotide
- <220>
- <221> misc feature
- <222> (1336)..(1336)
- <223> unknown nucleotide

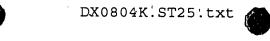
<220> <221> misc_feature <222> (1342)(1342) <223> unknown nucleotide															
<220> <221> misc_feature <222> (1369)(1369) <223> unknown nucleotide															
<400> 1 tcgacccacg cgtccgcgct gcgactcaga cctcagctcc aacatatgca ttctgaagaa 60															
agatggctga gatggacaga atgctttatt ttggaaagaa acaatgttct aggtcaaact 120															
gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca 170 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr															
		Me	t G1:	n Th	r Ph	e Thi	r Me	t Va	I Le	ı Glı	ı Gi	u Ile	e Tr	o Thr	
	1				5				10						
agt ctt	ttc	atg	tgg	ttt	ttc	tac	gca	ttg	att	cca	tgt	ttg	ctc	aca	
Ser Leu	ı Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	
15					20					25					
gat gaa 266	gtg	gcc	att	ctg	cct	gcc	cct	cag	aac	ctc	tct	gta	ctc	tca	
Asp Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser	
30				35					40					45	
acc aac	atg	aag	cat	ctc	ttg	atg	tgg	agc	cca	gtg	atc	gcg	cct	gga	
Thr Asn	Met	Lys	His	Leu	Leu	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro	Gly	

Page 2

55

60

50



gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg
362
Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
65
70
75

tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa 410

Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu

80 85 90

ggt cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac 458

Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr

95

100

105

aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc 506
Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser 110

atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct 554

Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro

130

135

140

ggg atg gag atc ncc aaa nat ggc ttc cac ctg gtt att gag ctg gag 602
Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu
145
150
155

gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag 650 Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu 160 165 170 DX0804K.ST25.txt

cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca 698 Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro 175 180 185

gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc 746 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala 190 195 200 205

cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca 794 Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr 210 215 220

gaa tgt gtg gar gtg caa gga gag occ att ccc ctg gta ctg gcc ctg
842
Glu Cys Val Glu Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu
225
230
235

ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc 890
Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe
240
245
250

gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg
938

Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val
255

260

265

gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc 986 Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile 270 275 280 285

agc tgc aga agg gag gtg gat gcc tgt gcc acg gct gtg atg tct 1034 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser

290 295 300

cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgcg gaagggccca 1084

Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser

305 310

ggtgaagccg agaacctggt ctgcatgaca tggaaaccat gaggggacaa gttgtgtttc 1144

tgttttccgc cacggacaag ggatgagaga agtaggaaga gcctgttgtc tacaagtcta 1204

gaagcaacca tcagaggcag ggtggtttgt ckaacagaac aaytgactga ggytakrggg 1264

gwtgtgacct ctagactktg ggstkscayt tgcwtggytg agcaaccctg ggaaaagtga 1324

cttcatccct tnggtccnaa gttttctcat ctgtaatggg ggatncctac aaaactg 1381

<210> 2

<211> 311

<212> PRT

<213> Homo sapiens

<220>

<221> misc feature

<222> (146)...(146)

<223> The 'Xaa' at location 146 stands for Thr, Ala, Pro, or Ser.

<220>

<221> misc feature

<222> (148)..(148)

<223> The 'Xaa' at location 148 stands for Asn, Asp, His, or Tyr.

```
DX0804K.ST25.txt
```

```
<220>
<221> misc feature
<222> (171)..(171)
<223>
       The 'Xaa' at location 171 stands for Arg, or Thr.
<220>
<221> misc feature
<222> (214)..(214)
<223>
       The 'Xaa' at location 214 stands for Arg, or Lys.
<220>
<221> misc feature
<222> (567)..(567)
<223>
      unknown nucleotide
<220>
<221> misc feature
<222> (573)..(573)
<223> unknown nucleotide
<220>
<221> misc feature
<222> (1336)..(1336)
<223> unknown nucleotide
<220>
<221> misc feature
<222> (1342)..(1342)
      unknown nucleotide
<223>
<220>
<221> misc feature
<222>
      (1369)..(1369)
      unknown nucleotide
<223>
<400>
       2
Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu Phe
1
                5
                                    10
                                                        15
Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val
            20
                                25
                                                    30
```

Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met

Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu

Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe 195 200 205

Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val 210 215 220

Glu Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe

DX0804K.ST25.txt

225 230 235 240

Val Gly Phe Met Leu Ile Leu Val Val Pro Leu Phe Val Trp Lys 245 250 255

Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Leu Pro 260 265 270

Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg 275 280 285

Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu 290 295 300

Leu Leu Arg Ala Trp Ile Ser 305 310

<210> 3

<211> 1244

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(694)

<223>

<400> 3

c cgg gtc gac cca cgc gtc cgc ctg gtt tcc ccc tgg ctg aca gtg cct 49 Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro

1 5 10 15

tgg ttc ctg tcc tgt tgg aat gtt acc att ggg cct cct gag agc atc 97
Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile

20 25 30

tgg gtg acg ccg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc
145
Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
35
40
45

ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay
193
Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Tyr
50
55
60

tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac
241
Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
65
70
75
80

tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa 289

Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln

85

90

95

gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agg ccc ggc 337
Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly

100 105 110

cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg 385

Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr

115

120

125

aag ctt caa caa gtc atc ctc atc gcc gtg gga gtc ttt ctg tcg ctg
433
Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
130
135
140

T25.txt

gcg gcg ctg gcg ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc 481 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly 145 150 155 160

ctg gtg aaa tac tgg ttt cac tct ccg cca agc atc cca tca caa atc 529
Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile

165 170 175

gaa gag tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac 577 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp 180 185 190

aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt
625
Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
195
200
205

gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc 673
Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
210 215 220

caa aac tot ggt gcg gto tgo tagootgtgg ggtaagggot otgagoogag 724 Gln Asn Ser Gly Ala Val Cys

225 230

gaagetgetg atgtecatgt cageaettta tggaateegg teeteeattt teetgteeee 784

aaaaggcccg tcagtgcctg tgaagatgta acgggtctca tgggggcgac aagcttattg

844

atttttttt tcaaactaag agttttctaa tcatacgcgt ttttagaata attctacaga 904

tatgtccccg aaagattaag atttctctta aacactaaaa agacatgtaa ttatttgtta 964

gcaaatgggc gtctggcacg cctctgacac tttttcgtca gcagccagga cacgaggtcc 1024

cctccttgat gaagcccctc gggcagacca tgtcacctgt cccagcctgc cccaagaagg 1084

gacattaagt ggcccttctt catatccaaa cacctggctt gaaatgtgat tagccctgta 1144

aatagtttca cagagattaa gccttttttt cccccaagtt aggaataaaa gactataatt 1204

aactttttaa aaaaaaaaa aaaaaaaaaa 1244

<210> 4

<211> 231

<212> PRT

<213> Homo sapiens

<400> 4

Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro 1 5 10 15

Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile 20 25 30

Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro 35 40 45

Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Tyr 50 55 60

Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn

65

70

75

80

Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln 85 90 95

Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly 100 105 110

Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr 115 120 125

Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu 130 135 140

Ala Ala Leu Ala Gly Cly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly 145 150 155 160

Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile 165 170 175

Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp 180 185 190

Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
195 200 205

Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr 210 215 220

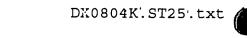
Gln Asn Ser Gly Ala Val Cys 225 230

<210> 5

<211> 337

<212> PRT

<213> Homo sapiens



<400> 5

Met Arg Pro Thr Leu Leu Trp Ser Leu Leu Leu Leu Gly Val Phe 1 5 10 15

Ala Ala Ala Ala Ala Pro Pro Asp Pro Leu Ser Gln Leu Pro Ala 20 25 30

Pro Gln His Pro Lys Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser 35 40 45

Trp Glu Pro Val Ala Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Arg 50 55 60

Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met 65 70 75 80

Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe 85 90 95

Thr Ala Ala Ser Pro Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr 100 105 110

Leu Arg Leu Arg Ala Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr 115 120 125

Met Pro Trp Phe Gln His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu 130 135 140

Asn Ile Glu Val Thr Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser 145 150 155 160

Ser Pro Phe Asp Ile Ala Asp Thr Ser Thr Ala Phe Phe Cys Tyr Tyr 165 170 175

Val His Tyr Trp Glu Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe 180 185 190

T25'.txt

Arg Ser Asn Ser Ile Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr 195 200 205

Cys Leu Gln Val Gln Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe 210 215 220

Arg Val Gly His Leu Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp 225 230 235 240

Ala Ser Thr Glu Leu Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe 245 250 255

Ser Leu Leu Ser Val Leu Ala Gly Ala Cys Phe Phe Leu Val Leu Lys 260 265 270

Tyr Arg Gly Leu Ile Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro 275 280 285

Leu Gln Ile Glu Glu Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu 290 295 300

Ala Leu Asp Lys Asp Ser Ser Pro Lys Asp Asp Val Trp Asp Ser Val 305 310 315 320

Ser Ile Ile Ser Phe Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr 325 330 335

Leu

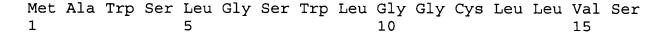
<210> 6

<211> 325

<212> PRT

<213> Homo sapiens

<400> 6



Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val 20 25 30

Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly 35 40 45

Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp 50 55 60

Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser 65 70 75 80

Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu 85 90 95

His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile 100 105 110

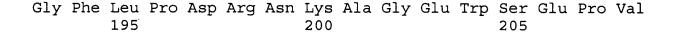
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His
115 120 125

Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr 130 135 140

Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys 145 150 155 160

Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu 165 170 175

Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg 180 185 190



Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala

Val Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly

Cys Phe Ser Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe

Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu Gly His

Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu

Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser

Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly

Gln Gly Pro Gln Ser